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objectives

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Chip Design

Querying and Mining
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Expression Analysis

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Scanning

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Exposure to Sample

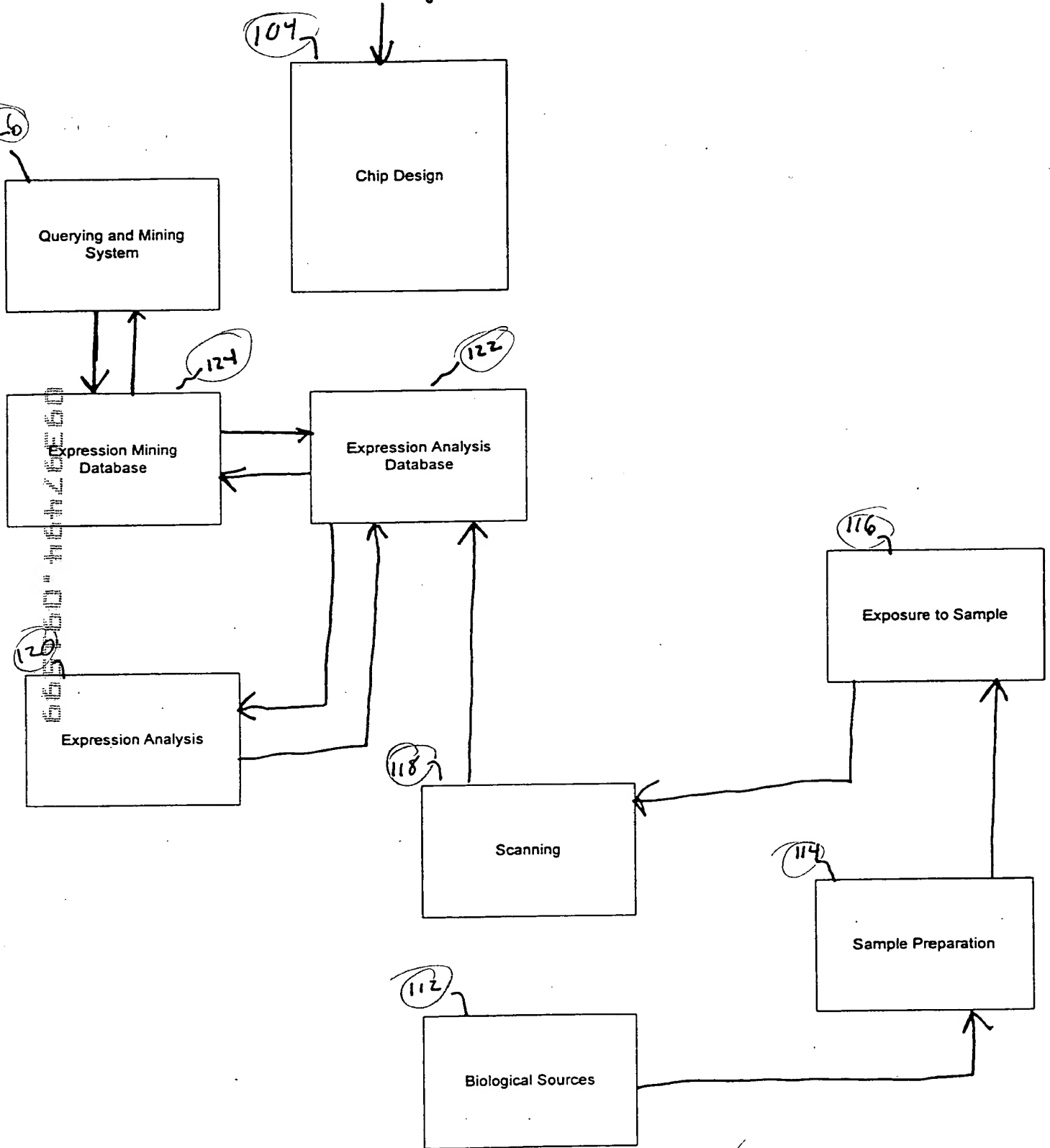
114

Sample Preparation

112

Biological Sources

Fig. 1



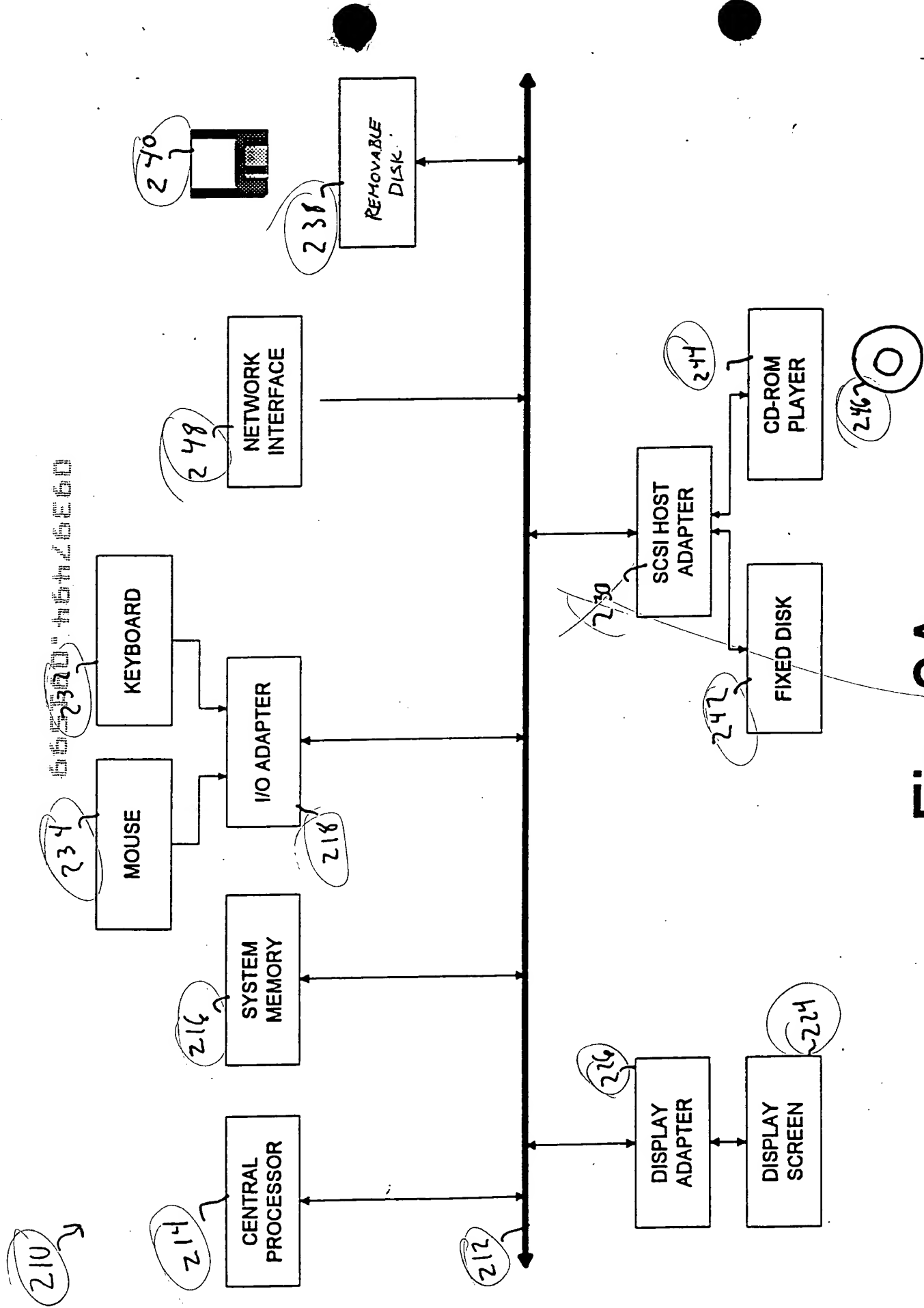


Fig. 2A

665T60"46H26E60

LAN

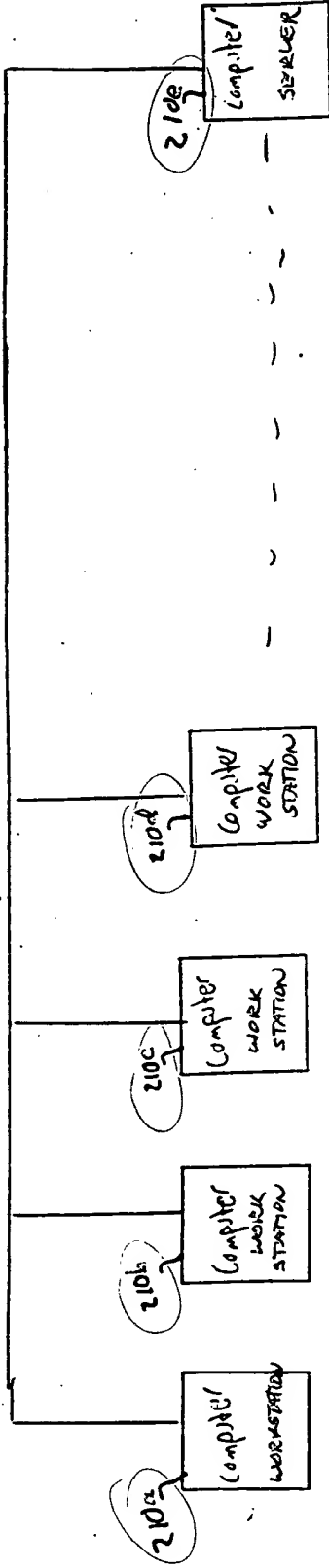


Fig. 2B

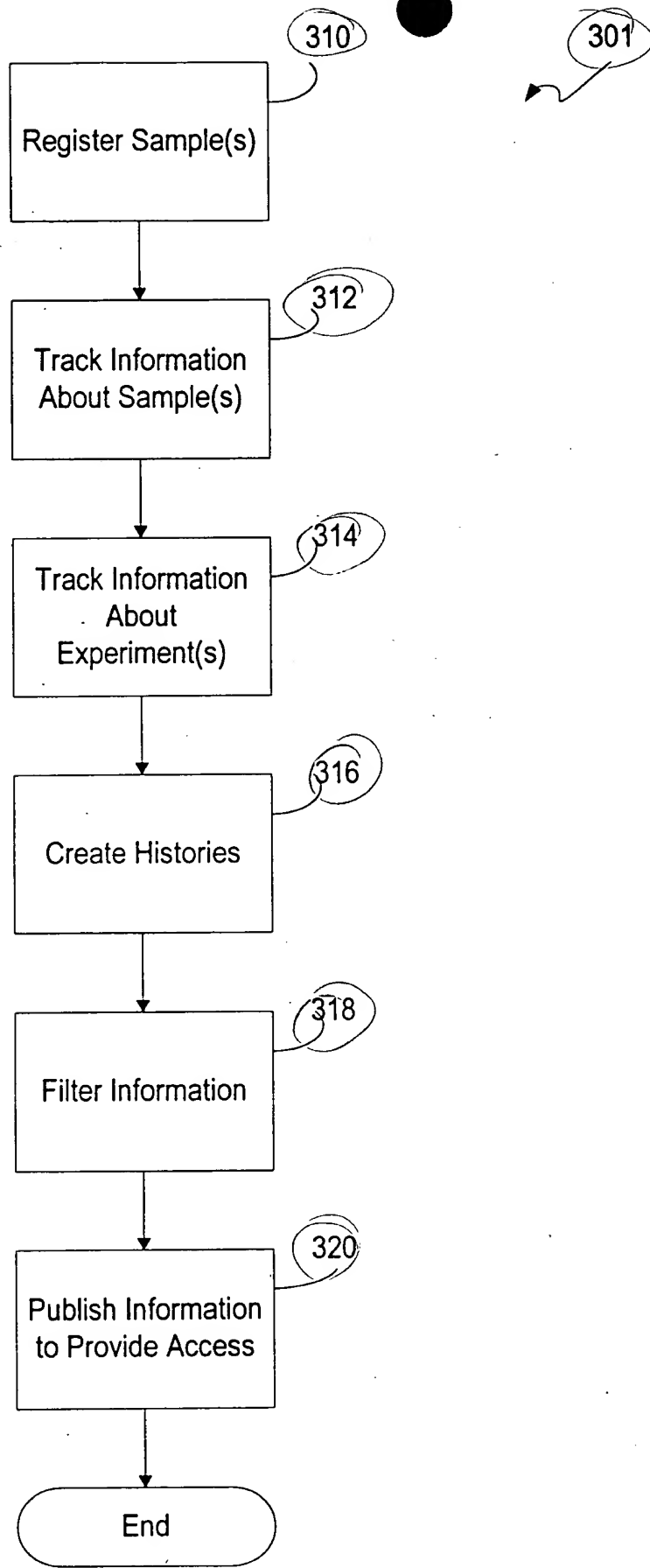


Fig. 3A

665760" 46426560

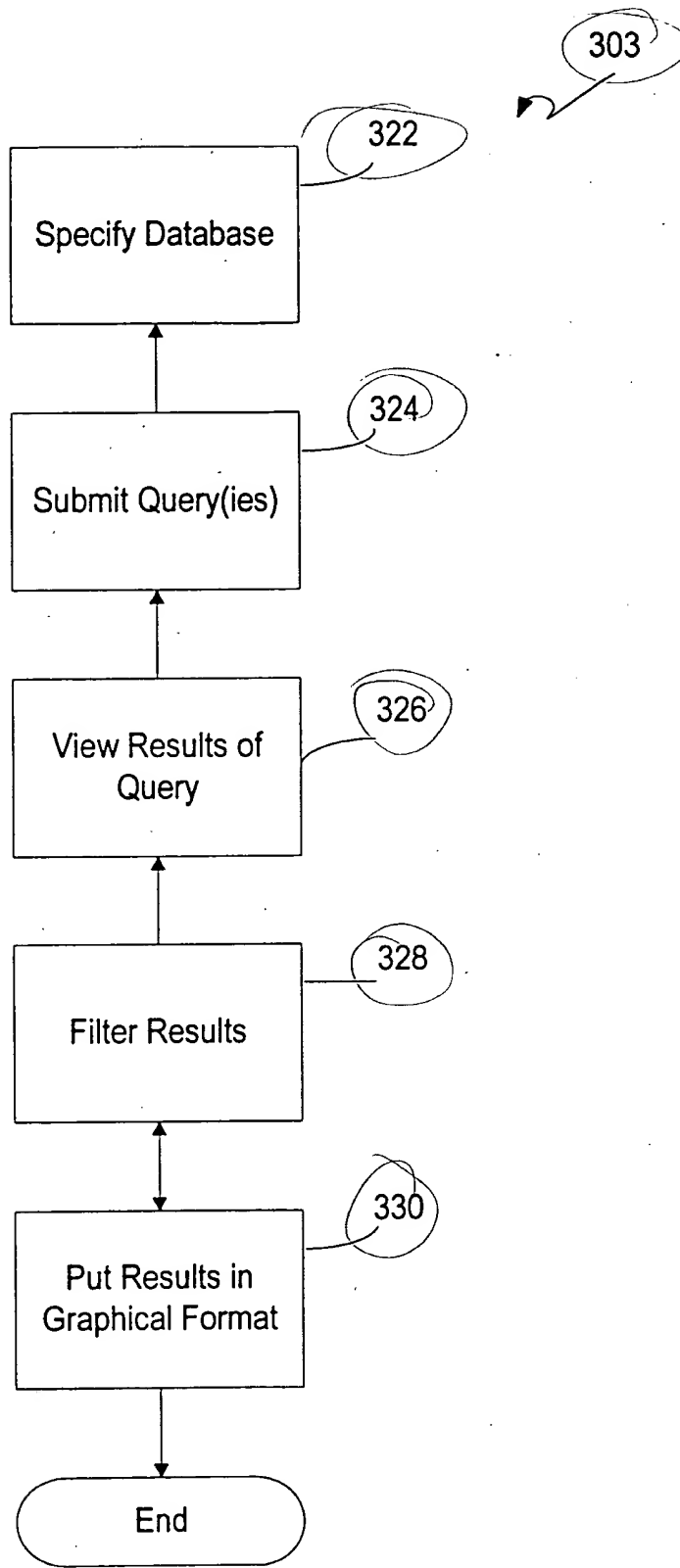


Fig. 3B

305

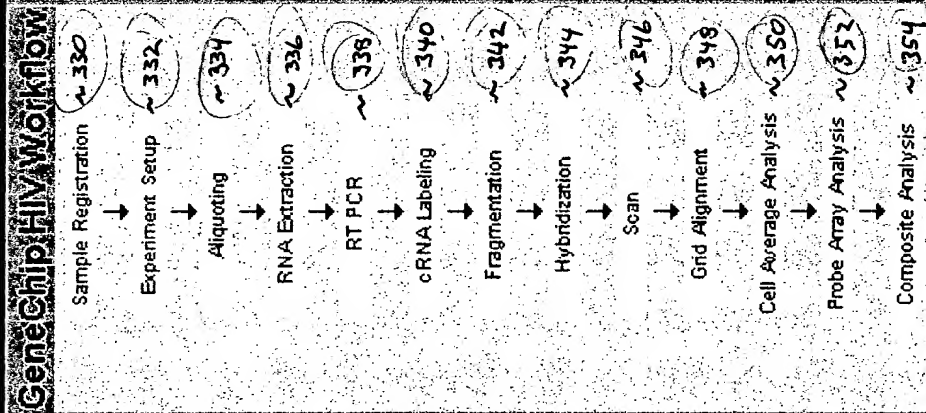


Fig. 3C

665760" +64/6660

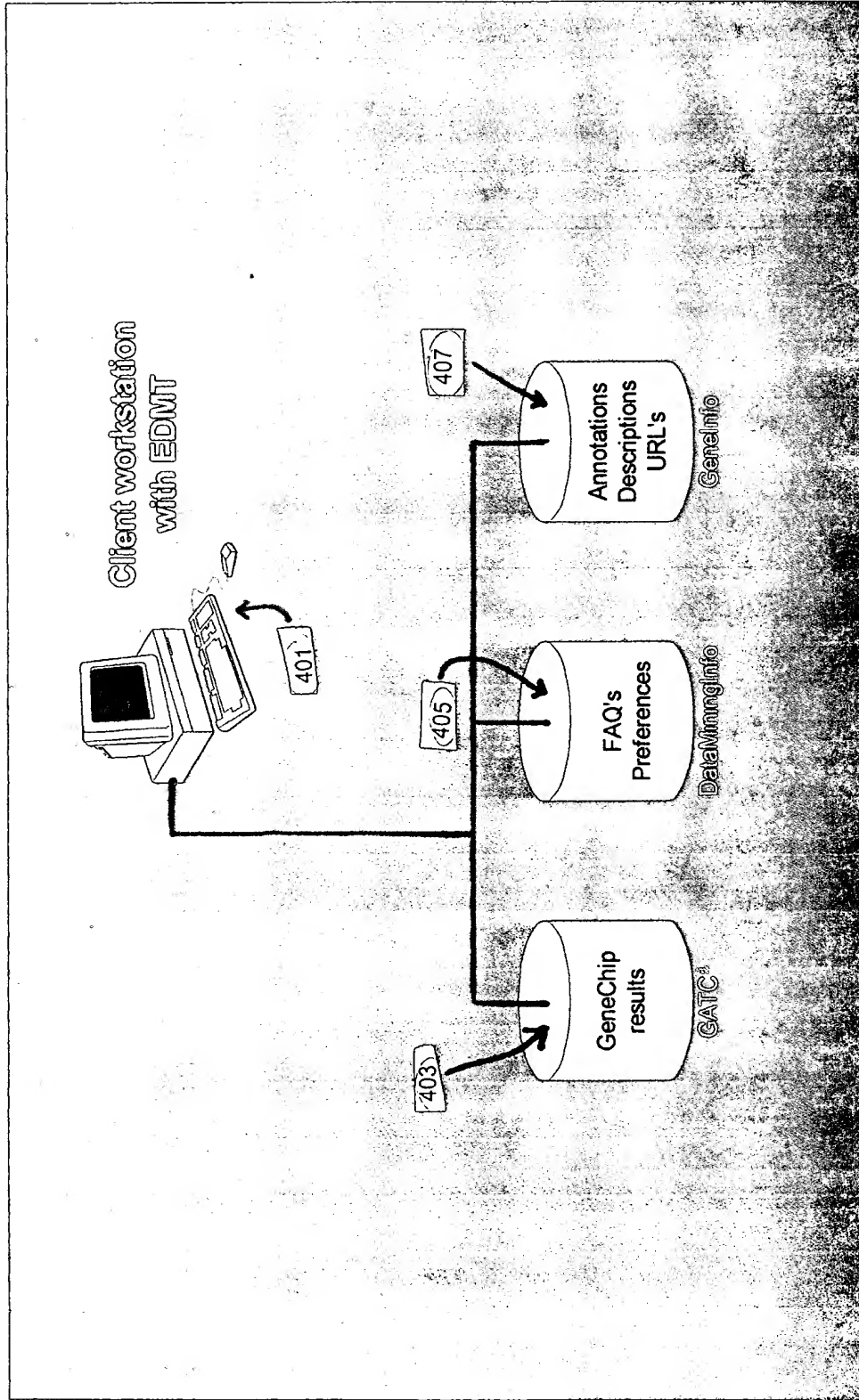


Fig. 4A

All DSN's on workstation
Currently selected DSN



4
50

GeneChip Expression Automation

Sample Info:

Sample name:

Sample type:

Sample project:

Description:

Comments:

Experiment Info:

Experiment name:

Probe Array Image ID:

Probe Array Types:

Probe Array Lot #:

Cell Average Set:

Probe Array Analysis Set:

Publish Database:

Automate Clear

Sample/Experiment/Probe array image ID:

Sample	Experiment	Probe array image ID
Demo	DemoEsubA	DemoCsubA
Demo	DemoEsubB	DemoCsubB
Demo	DemoEsubC	DemoCsubC
Demo	DemoEsubD	DemoCsubD
Demo1	Demo1EsubA	Demo1EsubB
Demo1	Demo1EsubC	Demo1EsubD

Multiple experiments per sample

Multiple samples

User parameter sets

Fig. 5A

503

Comments:

Cell Average Set:

Probe Array Analysis Set:

Publish Database:

Automate

Results

Result	Message
Pass	Sample Demo passed registration
Pass	Experiment DemoEsusbA passed automation
Pass	Sample Demo passed requere
Pass	Experiment DemoEsusbB passed automation
Pass	Sample Demo passed requere
Pass	Experiment DemoEsusbC passed automation
Pass	Sample Demo passed requere
Pass	Experiment DemoEsusbD passed automation
Pass	Sample Another Demo passed registration
Pass	Experiment Another DemoEsusbA passed automation
Pass	Sample Another Demo passed requere
Pass	Experiment Another DemoEsusbB passed automation
Pass	Sample Another Demo passed requere
Pass	Experiment Another DemoEsusbC passed automation
Pass	Sample Another Demo passed requere
Pass	Experiment Another DemoEsusbD passed automation

First Sample is registered

First Experiment setup

First Sample is re-queued

Second Experiment setup

Fig. 5B

50555TED46746E60

Filtered by sample project

GeneChip Expression Scan

Pending Scan

Hybridized Exp/Probe Array Image ID:

DemoEsubA/DemoCsubA
DemoEsubB/DemoCsubB
DemoEsubC/DemoCsubC
DemoEsubD/DemoCsubD

Sample/Experiment Info:

Sample Info:
Name: Demo
Project: Demo
Type: Blood
User: dbernth
Date: Aug 23 1998 12:36PM
Experiment Info:
Name: DemoEsubC

Hybridization Info:

Reagents: (null)
Lot Number: (null)
Comments: This is a comment

Sample projects:

Demo

Sample types:

Blood

Probe array types:

Probe Array Info:

Probe Array Image ID:
DemoCsubC
Probe Array Type: Hu6800subC
LotNumber: Lot # 12345

Probe Array Type:
Hu6800subC

Clear

Previous

Next

| Sample Registration | Experiment Setup | Hybridization | Scan | Grid Alignment | Cell Average Analysis | Probe Array Analysis |
Expression Workflow | Log out

Fig. 5C

GeneChip HIV Sample Registration

Sample name: HivDemo (602)

Sample project: HivDemo

Sample type: [v]

Description: This is a description

Comments: This is a comment

Initial stage: RNA Extraction

ID: 1 Vessel (604)

HivDemov

Registered samples: (606) (608)

Sample Info:

Register

Clear

Update...

History...

Next

Sample Registration

Experiment Setup

Aliquoting

RNA Extraction

RT PCR

cRNA Labeling

Fragmentation

Hybridization

Scan

Grid Alignment

Fragmentation

Hybridization

Scan

Cell Average Analysis

Probe Array Analysis

Composite Analysis

HIV Workflow | Log out

Fig. 6A

65750" 4642660

631

GeneChip HIV Grid Alignment

The grid was manually aligned and sent to cell averaging

Failed automatic grid alignment and is waiting on the queue

Pending GridAlignment

Experiment(s)/Probe Array(s)

Completed GridAlignment

Experiment(s)/Probe Array(s)

Sample Info:
Name - HivDemo
Project - HivDemo
Type - (null)
User - dbern
Date - Aug 23 1998 1:28PM
Experiment Info:
Name - HivDemoE

File Type Info:
Probe Array Image ID:
HivDemoCs
File Type: DAT
Name: HivDemoCs.DAT
User/Creator: dbern
Date/Date: Aug 24 1998

Probe Array Info:
Array Name: HivDemoCs
Array Type: PRT 440S
Lot/Number: Lot # 12345

Sample projects:
HivDemo

Sample types:

Probe array types:
PRT 440S

Grid Alignment:
Manual

Clear

Previous Next

Sample Registration | Experiment Setup | Aliquoting | RNA Extraction | PCR Labeling | RT - cRNA | Fragmentation | Hybridization | Sczn | Grid Alignment | Probe Analysis | Composite Analysis

HIV Workflow | Log out

Fig. 6D

GenoChip HIV Cell Average Analysis

Sample projects:

Experiment names:

Sample types:

Probe array types:

User names:

Cell Average Name:

Image Data/Probe Array Type:

Image Data Cell Data:

Algorithm:

Parameter:


Run:

Clear:

Defaults:

>>
<<

Results

Image Name	Cell Name	Probe Array Type	Parameters	Result
HivDemoCs.DAT	hivdemocs cel	prt 440s	Percentile=75 CellFileVersion=3 CellMargin=2 CellsY=145 CellsX=141	

Previous
Next

[Sample Registration](#) |
 [Experiment Setup](#) |
 [Aliquoting](#) |
 [RNA Extraction](#) |
 [RT-PCR](#) |
 [cRNA Labeling](#) |
 [Fragmentation](#) |
 [Hybridization](#) |
 [Scan](#) |
 [Grid Alignment](#) |
 [Probe Array Analysis](#) |
 [Composite Analysis](#)

[HIV Workflow](#) |
 [Log out](#)

Fig. 6E

GeneChip HIV Probe Array Analysis

Sample projects:

Experiment names:

Sample types:

Probe array types:

User names:

Probe array Name:

Probe Array Data:

Algorithm:

GeneChip Rules:

Parameters:

Run:

Clear:

Details:

Results

Cell Name	Probe Array Name	Probe Array Type	Parameters	Result (/Fail)
HivDemoCa CEL	hivdemoca.chp	prt 440a	Ratio=1.2 BOCutoff=15.0 BGSub=-1.0 IntraChipComposite=1	Pass
hivdemocs.cel	hivdemocs.chp	prt 440s	Ratio=1.2 BOCutoff=20.0 BGSub=-1.0 IntraChipComposite=1	Pass

Previous

Next

Sample Registration | Experiment Setup | Aliquoting | RNA Extraction | RT-PCR | cRNA Labeling | Fragmentation | Hybridisation | Scan | Grid Alignment | Cell Average Analysis | Probe Array Analysis | Composite Analysis

HIV workflow | Log out

Fig. 6F

GeneChip HIV Composite Analysis

Sample projects: HivDemo

Experiment names: HivDemoE

Sample types:

User names: dberrh

Sense/Antisense Probe Array:

Composite Data:

Algorithm: GeneChip Rules

Parameter: Hybrid

Buttons: Run Clear Defaults

Results

Sense Chip File Name: hivdemoE.chp

Antisense Chip File Name: hivdemoE.chp

Composite File Name: hivdemoE.chp

Parameters: hivdemoE.chp

Result: hivdemoE.chp

Buttons: Previous

Workflow: Sample Registration | Experiment Setup | Aliquoting | RNA Extraction | RT-PCR | cRNA Labeling | Fragmentation | Hybridization | Scan | Alignment | Grid | Coll. Average | Probe Array | Analysis | Composite Analysis

Workflow: HIV Workflow | Log out

Sample name: HivDemo

EXPERIMENT NAMES WITH COMPLETED PROCESSES:

- HivDemoE
- Sample Registration
- Experiment Setup
- Aliquoting
- RNA Extraction
- RT-PCR
- cRNA Labeling
- Fragmentation
- **Hybridization**
- Scan
- HivDemoCa.DAT
- HivDemoCs.DAT
- Grid Alignment
- HivDemoCa.DAT
- HivDemoCs.DAT
- Cell Average Analysis
- HivDemoCa.CEL

HivDemoE / Hybridization

> Vessel

- *ID: HivDemoELabsFig
- > Probe array
- *ID: HivDemoCs
- *Array type: PRT 440S
- *Lot #: Lot # 12345
- <Hyb Description 0
- *Date: Aug 24 1998 7:12:16AM
- *Name: PRT 440s
- *Reagents: Hiv sense reagent
- *Lot #: Lot #6789
- *Comments: Hiv sense Hyb comment
- *Description: (none)
- *Stages: Completed
- *Station ID: 0
- *Station #: 1
- *Module: 1

Print Preview...

Clear

Cancel

Sample Registration

Experiment Setup

RNA Extraction

RT-PCR

cRNA Labeling

Fragmentation

Hybridization

Scan

Grid Alignment

Cell Average Analysis

Cell

Probe Array

Composite Analysis

HIV Workflow | Log out

Fig. 6H

1990-1991

102

Probe array types: Hu6800subA 710

User names: dbernh 712

Algorithm: GeneChip Histogram 714

☐ Use set name in analysis

Cell Average Name: 716

Existing set name(s): 711

Parameter: 718 Modify

Percentile=75
CellFile/version=3
CellMargin=2

Run
Clear
Defaults
Create Set...

Create/Update set name: 713

Image Name	Cell Name	Probe Array Type	Algorithm	Set Name	Result ()
dbSubA0.dat	dbsuba0.cel	Hu6800subA	GeneChip Percentile	DerekDP0	
dbSubA1.dat	dbsuba1.cel	Hu6800subA	GeneChip Percentile	DerekDP0	
dbSubA10.dat	dbsuba10.cel	Hu6800subA	GeneChip Percentile	DerekDP0	
dbSubA11.dat	dbsuba11.cel	Hu6800subA	GeneChip Percentile	DerekDP1	
dbSubA12.dat	dbsuba12.cel	Hu6800subA	GeneChip Percentile	DerekDP1	
dbSubA13.dat	dbsuba13.cel	Hu6800subA	GeneChip Percentile	DerekDP1	

Fig. 7A

665760" 4642660

703

GeneChip Create Set Name

Go back to GeneChip Data Analysis page.

Probe Array Types:
Hu6800subA
Hu6800subB
Hu6800subC
Hu6800subD
1165ara
1165bra

720

Probe Array Types used:
Hu6800subA
Hu6800subB
Hu6800subC
Hu6800subD

722

Existing set name(s):
Derek0
Hu6800
JSteph1165ara1
newparam0
syah1
syah2
syah2

724

Create/Update set name:
Hu6800

Scaling | Normalization | ProbeMask | Baseline

☒ Use Baseline Comparison File

Bartel36IMG.CHP
ltest1a.chp
lhuman_a1.CHP
dbsub10.chp
dbsub10.chp

720

Parameter:
30.00

Modify

Horizontal Zones=4
Vertical Zones=4
%BG Cells=80
STP=3.00
Ratio Threshold=1.50
Ratio Limit=10.00
Abs Pos/Neg Min=3.00
Abs Pos/Neg Max=4.00
Abs Pos/Tot Min=0.33
Abs Pos/Tot Max=0.43
Abs Avg Ratio Min=0.90

724

Update Set

Clear

Defaults

Multiple probe array types per parameter set

New set

Fig. 7B

Assay type

Data type

Probe array type

Month / Day / Year

Sample project

Experiment name

Sample type

User name

GeneChip Expression Cell Data Analysis

Go back to GeneChip Data Analysis Filter page.

Sample projects: ExpMig

Experiment names: dbSubA1

Sample types: ExpMig

Probe array types: Hu6800subA

User names: dberrh

Cell Data/Probe Array Type: Cell Data/Probe Array Type

Probe Array Name: dbsuba1.chp

Algorithm: Robust Multi-array Average (RMA)

Scaling | Normalization | ProbeMask | Baseline | Parameters

SDT Multiplier: 35.00 Modify

Horizontal Zones=4

Vertical Zones=4

%BG Cells=80

STP=3.00

Ratio Threshold=1.50

Ratio Limit=10.00

Abs Pos/Neg Min=3.00

Abs Pos/Neg Max=4.00

☐ Use set name in analysis

Existing set name(s):

Create/Update set name:

Cell Data/Probe Array Name:

Run Clear Defaults Create Set...

Fig. 7C

655746746E602

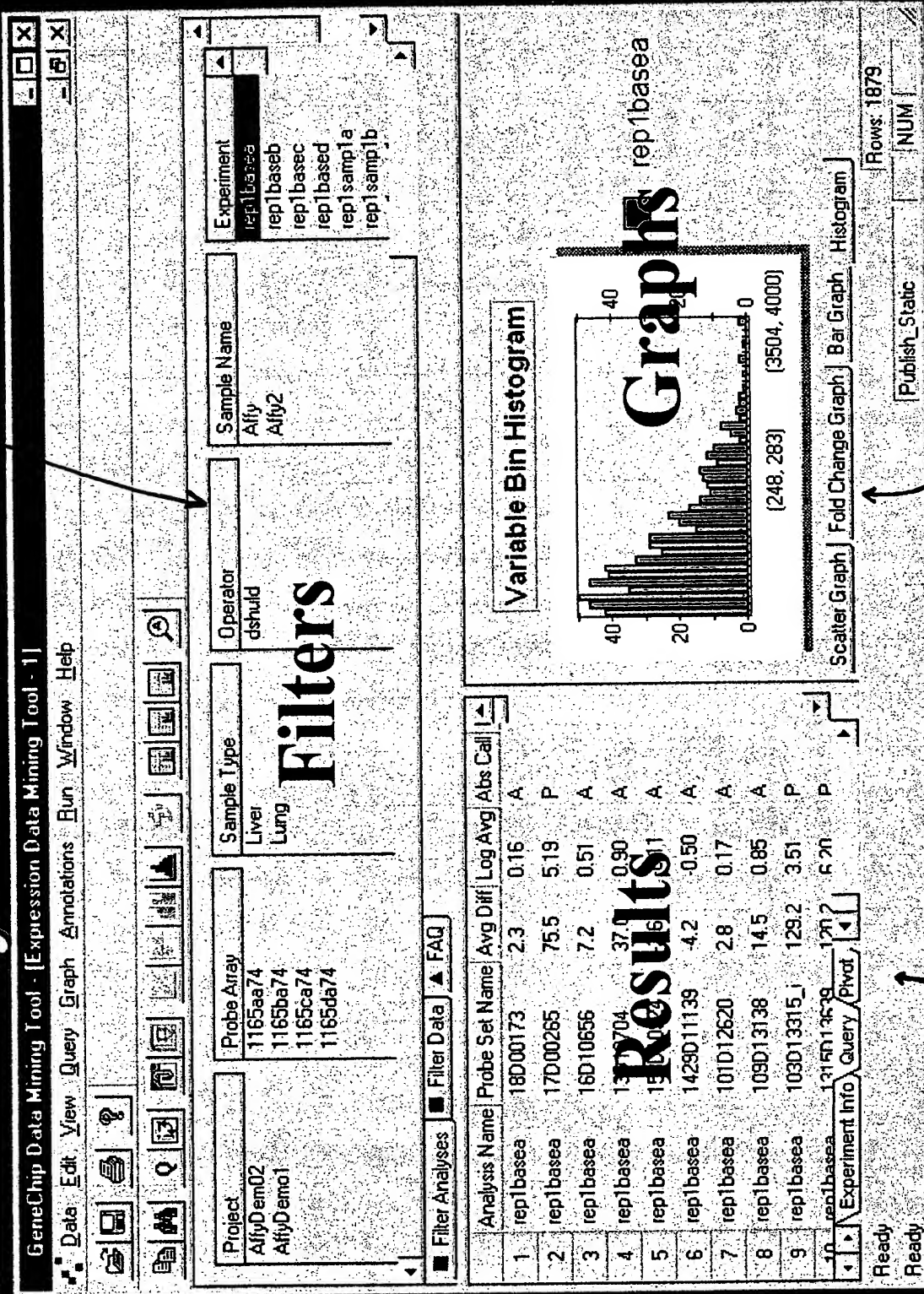


Fig. 8A

802

Filter results

Diff Call	Probe Set Name	Avg Diff	Abs Call	Positive	Negative	Pairs	Pairs Used	Inc InAvail	Inc Avail	PM Excess	MM Excess	Inc Dec	Inc Ratio	Dec Ratio
		Descending												
		>20	=P											

Build Avg Diff Filter

1

=

<

>

(

)

And

Or

%

Like

In

Between

Not

Undo

Fig. 8B

665T60" h5h/6660

Experiment results table

Query results table

Pivot results table

		rep1basea		rep1sample	
Project		AlfyDemo1		AlfyDemo1	
Probe Array		1165aa74		1165aa74	
Sample Type		Lung		Lung	
Operator		dshuld		dshuld	
AUG					
Analysis Name	Probe Set Name	Avg Diff	Log Avg	Abs Call	
1 rep1basea	18D00173	2.3	0.16	A	
2 rep1basea	17D00265	75.5	5.19	P	
3 rep1basea	16D10656	7.2	0.51	A	
4 rep1basea	13D10704	37.0	0.90	A	
AUG					
		rep1basea		rep1sample	
		Avg Diff	Abs Call	Avg Diff	Abs Call
18D00173		2.3	A	0.9	A
17D00265		75.5	P	66.5	P
16D10656		7.2	A	0.4	A
13D10704		37.0	A	26.8	A
158D10924		2.6	A	3.6	A
1429D11139		4.2	A	0.2	A
101D12620		2.8	A	4.8	A
109D13138		14.5	A	29.1	P
103D13315_1		129.2	P	216.9	P
1315D13639		120.2	P	90.9	P
108D13665		8.4	A	1.6	A
AUG					
Experiment Info		Query		Pivot	

Fig. 8C

- Graph any numeric results
- Log or linear scale
- Multiple analyses per axes
- Description of probe set
- Hot link to external database (Entrez)
- Roping to filter pivot table
- Options (point size, color, size)

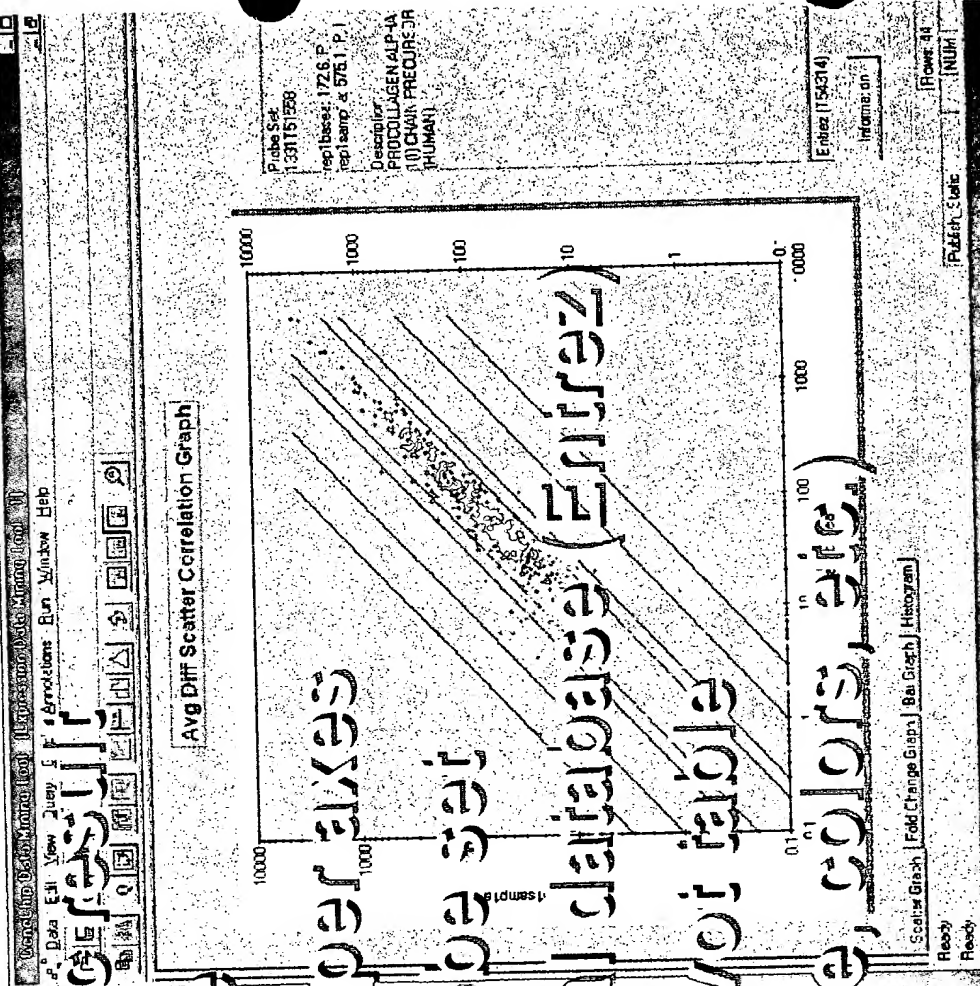


Fig. 8D

Fig. 8E

665T60"4642660

Graph any numerical
Options (bar size,

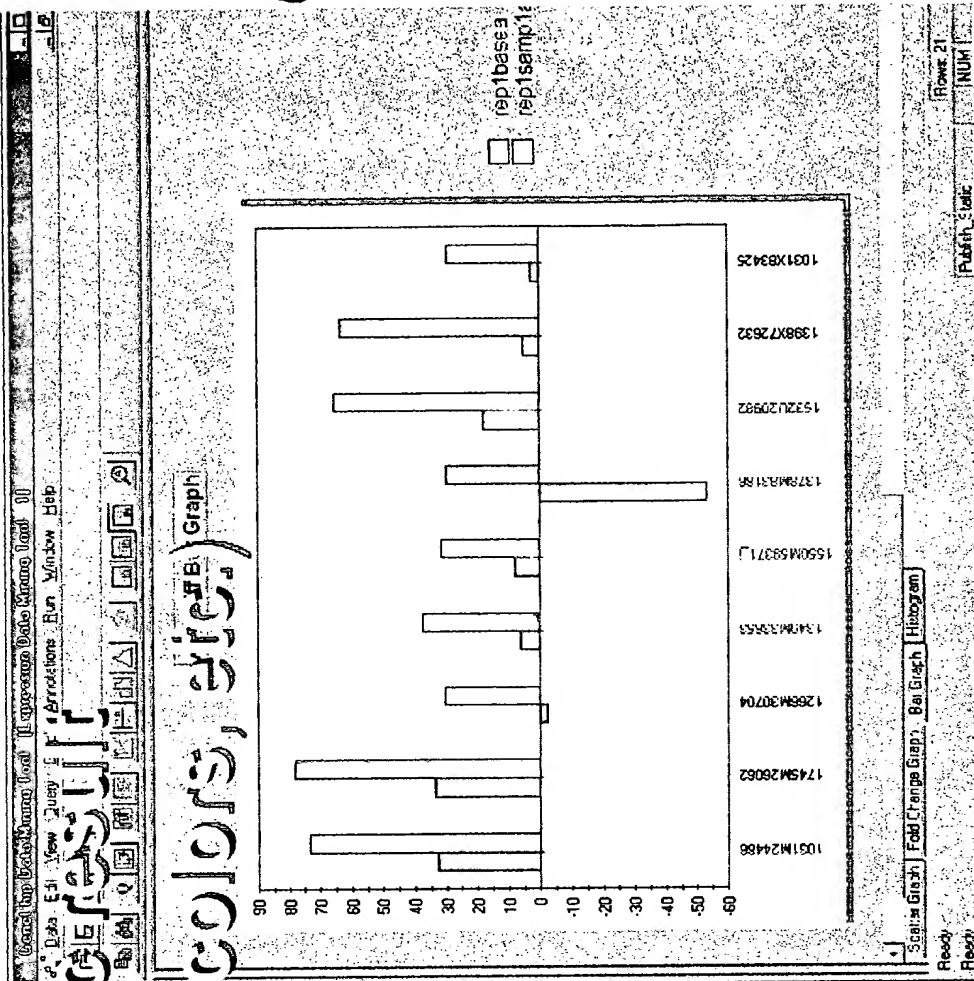


Fig. 8F

Histogram Graph

- Histogram of average difference
- Landmarks
- Options (bin size, range, colors, etc.)

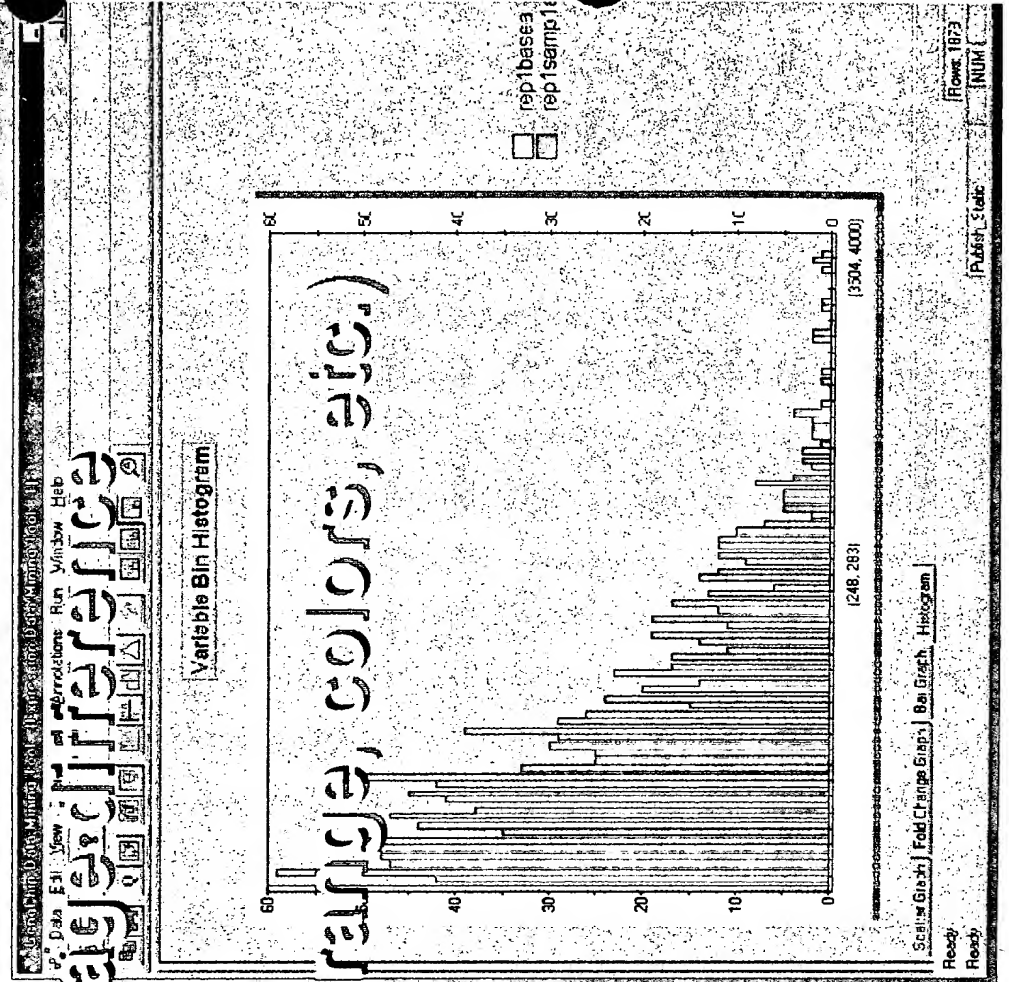


Fig. 8G

USPTO 4646600

Filters saved to DataMiningInfo database

Name saved queries

Save

foo	NewlySavedQuery	show
Highly expressed genes	NewlySavedQuery2	t1
lcl1	one	t11
ll	query	t2
ll test	read-only	t22
ll1	read-only2	t23
My favorite query	ro	t3
network	save1	test1
new	scatter	test2

Name:

☐ Only show my queries.

☐ Show save changes dialog.

Save Cancel

Fig. 9A

Annotate probe set(s)

Annotations include

- Annotation text
- Type (user defined)
- User name
- Date of annotation

Annotate

Probe Set(s): 109D13136

Annotation Type: Classification

Annotation: The function of this gene is to ...

OK Cancel

903

Fig. 9B

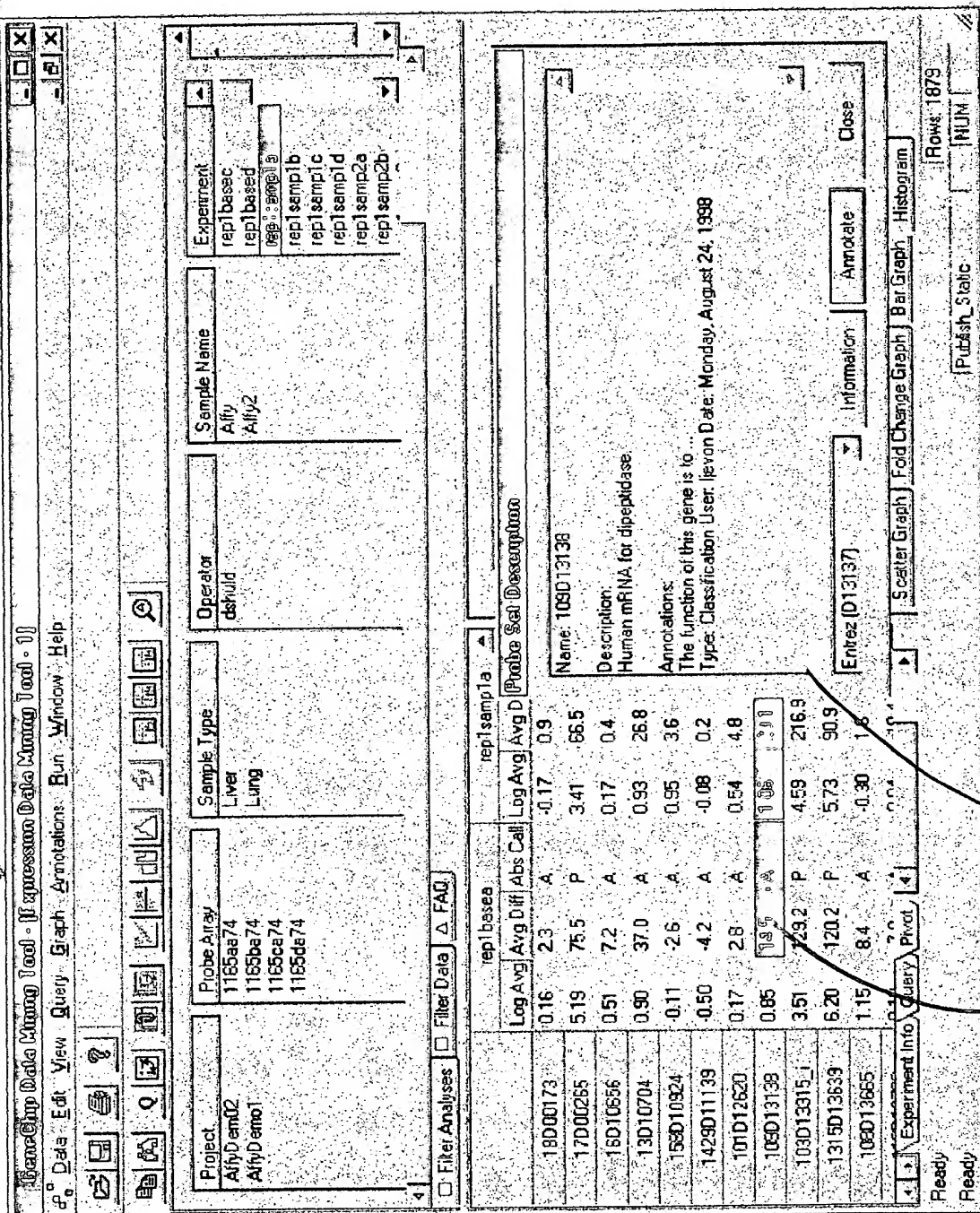


Fig. 9C

Specify multiple constraints (filters)
Update annotations (owner only)

Uniqy Annotations					
Field	Search For	Operation	Date	User	Description
Probe Set	109D	AND			
Classification	function	AND			
>>					
Probe Set	Type	Annotation	Date	User	Description
1	109D13138	Classification	The function of this gene is to	levon	8/24/98 4:02:21 PM Human mRNA for dipeptidase

Fig. 9D

Fig. 9E

Probe Set Description

Name: 109D13138

Description:
Human mRNA for dipeptidase

Annotations:
The function of this gene is to
Type: Classification User: levon Date: Monday, August 24, 1998

Entrez (D13137) Information Annotate Close

Probe Set Description dialog

Browser Window

GenBank Data Entry Tool (Internet Browser)

Data Edit View Window Help

Back Forward Stop Refresh LMS

NCBI Entrez Nucleotide Query ELAST Entrez ?

Other Formats: FASTA Graphic

LOCUS HUMDP10 380 bp DNA PRI 03-APR-1993

DEFINITION Human dipeptidase gene, exon 1C.

ACCESSION D13137

KEYWORDS dipeptidase.

SOURCE Homo sapiens liver DNA, clone lib:genomic library.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 380)

AUTHORS Satoh,S., Kusumaki,C., Kenta,Y., Niva,E. and Kohsaka,X.

TITLE Cloning and structural analysis of genomic DNA for human renal dipeptidase

JOURNAL Biochim. Biophys. Acta 1172 (1-2), 18-183 (1993)

MEDLINE 93176806

REFERENCE 2 (bases 1 to 380)

AUTHORS Satoh,S.

TITLE Direct Submission

JOURNAL Submitted (01-SEP-1992) to the DDBJ/EMBL/GenBank databases. Submission

For Help, press F1

NUM

Fig. 10A

GeneChip Migration Tool

d:\genechip\testdata\

Local Files

EXP | CEL | CHP | CMP |

1165A_BASE.EXP

3106.EXP

88CP28-500.EXP

GP53A.EXP

p450.exp

P53A.EXP

1024

Create Sample

Data To Migrate

Migration Samples

3-30-98-1

MySample

1165A_EXP.EXP

1165A_EXP.CEL

MyHIVSample

440i

440i-1a.EXP

440i-1a.cel

440i-1a.CHP

440i-1s.exp

440i-1s.CEL

440i-1s.CHP

440i-comp.CMP

1026

Status

Sample: human

Sample Type: genomic DNA

Project: human

Workflow: Expression

Server: levon

Description: (null)

1028

LIMS Samples

1 sample

11

human

test1

newt1

newt10

1030

Sample Filters

Workflow

Expression

Sample Type

Project

Show all samples

Migrate

Close

Browse

View Log

Fig. 10C

665760"464/5E60

1031

Fluores Station-1

#	Experiment Name	Probe Array Type	Protocol	Current Stage	Time/Cycle	Temp	Close
1	1165A BASE	1165ARA	EMERGEWS1				Run
2	[No Probe Array]						Run
3	[No Probe Array]						
4	[No Probe Array]						

Fluores Station 1

Assay Types: Expression

Experiments: [v]

Probe Array Types: [v]

Protocols: EMERGEWS1

Vessel Bar Code: TEADISE

Probe Array Lot: 71449

Probe Array Image ID: 000Ahigh

Hybridized Experiments: 000Ahigh

Reagent Lot: 710812-04

Sample Projects: [All Projects]

Reagents: [v]

Users: [v]

Comments: 15nov/97

Module: 1 2 3 4

Hybridization Run

Experiment: [v]

Probe Array Type: [v]

Protocol: [v]

Current Stage: [v]

Time/Cycle: [v]

Temp: [v]

Run

Clear

Refresh

Close

File Mode

LIMS Mode

Fig. 10D

1041 COSTCO 1942425E50

Scanner

Experiment Name: 1165A_BASE

Probe Array Type: 1165ARA

Data File Location: d:\genetechip\testdata

Number of Scans: 4

Scanned Experiments: 1165A_BASE, 1165A_EXP, p450, P53A

Start Options... Laser ON Cancel

File Mode

Scanner

Assay Types: Expression

Experiments: human_a2, human_a3, human_a4

Sample Projects: [All Projects]

Users: lievon

Probe Array Image ID: 000Ahigh

Comments: 15nov97

Probe Array Type: 1228a71a

Number of Scans: 1

Data File Location: \\\DBSERVER02\GCLIMS\Data

Start Options... Laser ON Cancel

LIMS Mode

Fig. 10E

1051
1052

Experiment Information	
Data File Location:	d:\geneschip\testdata
Experiment Name:	P53A
Current Experiments:	<div> <div>3106</div> <div>440lj-1a</div> <div>440lj-1s</div> <div>88CP28-500</div> </div>
Scanned Experiments:	<div> <div>1165A_BASE</div> <div>1165A_EXP</div> <div>p450</div> <div>P53A</div> </div>
Probe Array Type:	GP53
Probe Array Lot:	601500.6#516
Operator Name:	JHC
Sample Type:	DNA
Sample Description:	Flourescein
Sample Project:	p53
Comments:	
Reagents:	3x
Reagent Lot:	
<div> <div>Save</div> <div>Clear</div> <div>Print</div> <div>Delete</div> </div>	
<div> <div>Edit</div> <div>< Back</div> <div>Next ></div> <div>Close</div> </div>	

File Mode

Experiment Information	
Data File Location:	\\DBSERVER02\GCLIMS\Data
Experiment Name:	000Ahigh
Current Experiments:	<div> <div>ihuman_a2</div> <div>ihuman_a3</div> <div>ihuman_a4</div> <div>ip53c</div> </div>
Scanned Experiments:	<div> <div>000Ahigh</div> <div>000Bhigh</div> <div>000Chigh</div> <div>000Dhigh</div> </div>
Assay Types:	[All Types]
Sample Projects:	[All Projects]
Users:	lievon
Probe Array Type:	1228a71a
Probe Array Lot:	71449
Operator Name:	lievon
Sample Type:	cDNA, ds
Sample Description:	
Sample Project:	Yeast
Comments:	[null]
Reagents:	
Reagent Lot:	710812-04
<div> <div>View</div> <div>Print</div> <div>< Back</div> <div>Next ></div> <div>Close</div> </div>	

LIMS Mode

Fig. 10F